

Sequence 1	lcl seq_1	Length	459	(1 .. 459)
Sequence 2	lcl seq_2	Length	440	(1 .. 440)
Identities = 412/459 (89%)				
Query: 1	MSAGWFRRRFLPGEPLPAPRPPGPHASVPVYRRPRFLRGSSSSPGAADASRRPDSRPVRS	60		
Sbjct: 1	MSAGWFRRRFLPGEPLPAPRPPGPHASVPVYRRPRFLRGSSSSPGAADASRRPDSRPVRS	60		
Query: 61	PARGRTLPNWAGYAEI INAEKSEFNEDQAACGKLCIRRCFEGAEIEWLTLCPEEFLTGHY	120		
Sbjct: 61	PARGRTLPNWAGYAEI INAEKSEFNEDQAACGKLCIRRCFEGAEIEWLTLCPEEFLTGHY	120		
Query: 121	WALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLNRCICPSDPQFVEEK	180		
Sbjct: 121	WALFDGHGGPAAAILAANTLHSCLRRLQLEAVVEGLVATQPPMHLNRCICPSDPQFVEEK	180		
Query: 181	GIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAIL	240		
Sbjct: 181	GIRAEDLVIGALESASFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAIL	240		
Query: 241	VRRDEIRPLSFEFTPETERQRIQQALFVYPELLAGEFTRLEFPRLKGGDDLQKVLFRDH	300		
Sbjct: 241	VRRDEIRPLSFEFTPETERQRIQQALFVYPELLAGEFTRLEFPRLKGGDDLQKVLFRDH	300		
Query: 301	HMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSV	360		
Sbjct: 301	HMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSV	360		
Query: 361	PQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQEDPHRFSK	415		
Sbjct: 361	PQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSLPGNQE+P + K	415		
Query: 416	LAQMILIHSTQGKEDSLTEEGQVSYDDVSFVIPLHSQGQESSDH	459		
Sbjct: 416	AGPDADTQHTGKGRQSHRGRAGVLR	440		